

=====

Sequence Listing was accepted.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: MSpencer

Timestamp: Mon May 07 11:46:59 EDT 2007

=====

Application No: 10593811 Version No: 1.0

Input Set:

Output Set:

Started: 2007-04-20 12:04:03.761
Finished: 2007-04-20 12:04:04.552
Elapsed: 0 hr(s) 0 min(s) 0 sec(s) 791 ms
Total Warnings: 28
Total Errors: 0
No. of SeqIDs Defined: 44
Actual SeqID Count: 44

ErrCode	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (16)
W 213	Artificial or Unknown found in <213> in SEQ ID (17)
W 213	Artificial or Unknown found in <213> in SEQ ID (18)
W 213	Artificial or Unknown found in <213> in SEQ ID (19)
W 213	Artificial or Unknown found in <213> in SEQ ID (20)
W 213	Artificial or Unknown found in <213> in SEQ ID (21)
W 213	Artificial or Unknown found in <213> in SEQ ID (22)
W 213	Artificial or Unknown found in <213> in SEQ ID (23)
W 213	Artificial or Unknown found in <213> in SEQ ID (24)
W 213	Artificial or Unknown found in <213> in SEQ ID (25)
W 213	Artificial or Unknown found in <213> in SEQ ID (26)
W 213	Artificial or Unknown found in <213> in SEQ ID (27)
W 213	Artificial or Unknown found in <213> in SEQ ID (28)
W 213	Artificial or Unknown found in <213> in SEQ ID (29)
W 213	Artificial or Unknown found in <213> in SEQ ID (30)
W 213	Artificial or Unknown found in <213> in SEQ ID (31)
W 213	Artificial or Unknown found in <213> in SEQ ID (32)
W 213	Artificial or Unknown found in <213> in SEQ ID (33)
W 213	Artificial or Unknown found in <213> in SEQ ID (34)
W 213	Artificial or Unknown found in <213> in SEQ ID (35) This error has occurred more than 20 times, will not be displayed

SEQUENCE LISTING

<110> Okamoto, Kiyoshi
Kawamura, Takanori
Asano, Makoto
Shitakubo, Daiya
Shirato, Manabu
Asada, Makoto

<120> Using non-human animal model, method of measuring transcription activity, method of measuring cell number and method of measuring tumor volume.

<130> 296514US0PCT

<140> 10593811
<141> 2007-05-07

<150> 10/593,811
<151> 2006-09-22

<150> PCT/JP05/005257
<151> 2005-03-23

<150> Japan 2004-084810
<151> 2004-03-23

<160> 44

<170> PatentIn version 3.3

<210> 1
<211> 24
<212> DNA
<213> Homo sapiens

<400> 1
catacgtggg ctccaaacagg tcct

24

<210> 2
<211> 24
<212> DNA
<213> Homo sapiens

<400> 2
cctacgtgct gtctcacaca gcct

24

<210> 3
<211> 24
<212> DNA
<213> Homo sapiens

<400> 3
cgcacgtggc cccggacacg cagc

24

<210> 4
<211> 24
<212> DNA
<213> Homo sapiens

<400> 4
cacacgtggg ttccgcacg tccg

24

<210> 5
<211> 8
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(8)
<223> IL4RE

<400> 5
tnnnnaa

8

<210> 6
<211> 9
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(9)
<223> IL4RE

<400> 6
tnnnnnnaa

9

<210> 7
<211> 10
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(10)
<223> IL4RE

<400> 7
tnnnnnnnnaa

10

<210> 8

<211> 10
 <212> DNA
 <213> Homo sapiens

<400> 8
 ttcccaagaa 10

<210> 9
 <211> 197
 <212> DNA
 <213> Simian virus 40

<400> 9
 tgcatactcaa ttagtcagca accatagtcg cggcccttaac tccgcccattt ccggccctaa 60
 ctccgccccag ttccgccccat tctccgcccc atggctgact aattttttt atttatgcag 120
 aggcccgaggc cgccctggcc tctgagctat tccagaagta gtgaggaggc ttttttggag 180
 gcctaggctt ttgcaaa 197

<210> 10
 <211> 1521
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(1518)

<400> 10
 atg ctg ctg ctg ctg ctg ggc ctg agg cta cag ctc tcc ctg 48
 Met Leu Leu Leu Leu Leu Leu Gly Leu Arg Leu Gln Leu Ser Leu
 1 5 10 15

ggc atc atc cca gtt gag gag gag aac ccg gac ttc tgg aac cgc gag 96
 Gly Ile Ile Pro Val Glu Glu Asn Pro Asp Phe Trp Asn Arg Glu
 20 25 30

gca gcc gag gcc ctg ggt gcc gcc aag aag ctg cag cct gca cag aca 144
 Ala Ala Ala Leu Gly Ala Ala Lys Lys Leu Gln Pro Ala Gln Thr
 35 40 45

gcc gcc aag aac ctc atc atc ttc ctg ggc gat ggg atg ggg gtg tct 192
 Ala Ala Lys Asn Leu Ile Ile Phe Leu Gly Asp Gly Met Gly Val Ser
 50 55 60

acg gtg aca gct gcc agg atc cta aaa ggg cag aag aag gac aaa ctg 240
 Thr Val Thr Ala Ala Arg Ile Leu Lys Gly Gln Lys Lys Asp Lys Leu
 65 70 75 80

ggg cct gag ata ccc ctg gcc atg gac cgc ttc cca tat gtg gct ctg 288
 Gly Pro Glu Ile Pro Leu Ala Met Asp Arg Phe Pro Tyr Val Ala Leu
 85 90 95

tcc aag aca tac aat gta gac aaa cat gtg cca gac agt gga gcc aca		336
Ser Lys Thr Tyr Asn Val Asp Lys His Val Pro Asp Ser Gly Ala Thr		
100	105	110
 gcc acg gcc tac ctg tgc ggg gtc aag ggc aac ttc cag acc att ggc		384
Ala Thr Ala Tyr Leu Cys Gly Val Lys Gly Asn Phe Gln Thr Ile Gly		
115	120	125
 ttg agt gca gca gcc cgcc ttt aac cag tgc aac acg aca cgc ggc aac		432
Leu Ser Ala Ala Ala Arg Phe Asn Gln Cys Asn Thr Thr Arg Gly Asn		
130	135	140
 gag gtc atc tcc gtg atg aat cgg gcc aag aaa gca ggg aag tca gtg		480
Glu Val Ile Ser Val Met Asn Arg Ala Lys Lys Ala Gly Lys Ser Val		
145	150	155
 gga gtg gta acc acc aca cga gtg cag cac gcc tcg cca gcc ggc acc		528
Gly Val Val Thr Thr Arg Val Gln His Ala Ser Pro Ala Gly Thr		
165	170	175
 tac gcc cac acg gtg aac cgc aac tgg tac tcg gac gcc gac gtg cct		576
Tyr Ala His Thr Val Asn Arg Asn Trp Tyr Ser Asp Ala Asp Val Pro		
180	185	190
 gcc tcg gcc cgc cag gag ggg tgc cag gac atc gct acg cag ctc atc		624
Ala Ser Ala Arg Gln Glu Gly Cys Gln Asp Ile Ala Thr Gln Leu Ile		
195	200	205
 tcc aac atg gac att gac gtg atc cta ggt gga ggc cga aag tac atg		672
Ser Asn Met Asp Ile Asp Val Ile Leu Gly Gly Arg Lys Tyr Met		
210	215	220
 ttt ccc atg gga acc cca gac cct gag tac cca gat gac tac agc caa		720
Phe Pro Met Gly Thr Pro Asp Pro Glu Tyr Pro Asp Asp Tyr Ser Gln		
225	230	235
 ggt ggg acc agg ctg gac ggg aag aat ctg gtg cag gaa tgg ctg gcg		768
Gly Gly Thr Arg Leu Asp Gly Lys Asn Leu Val Gln Glu Trp Leu Ala		
245	250	255
 aag cgc cag ggt gcc cgg tat gtg tgg aac cgc act gag ctc atg cag		816
Lys Arg Gln Gly Ala Arg Tyr Val Trp Asn Arg Thr Glu Leu Met Gln		
260	265	270
 gct tcc ctg gac ccg tct gtg acc cat ctc atg ggt ctc ttt gag cct		864
Ala Ser Leu Asp Pro Ser Val Thr His Leu Met Gly Leu Phe Glu Pro		
275	280	285
 gga gac atg aaa tac gag atc cac cga gac tcc aca ctg gac ccc tcc		912
Gly Asp Met Lys Tyr Glu Ile His Arg Asp Ser Thr Leu Asp Pro Ser		
290	295	300
 ctg atg gag atg aca gag gct gcc ctg cgc ctg ctg agc agg aac ccc		960
Leu Met Glu Met Thr Glu Ala Ala Leu Arg Leu Leu Ser Arg Asn Pro		
305	310	315
 320		

cgc ggc ttc ttc ctc ttc gtg gag ggt ggc atc gac cat ggt cat		1008	
Arg Gly Phe Phe Leu Phe Val Glu Gly Gly Arg Ile Asp His Gly His			
325	330	335	
cat gaa agc agg gct tac cgg gca ctg act gag acg atc atg ttc gac		1056	
His Glu Ser Arg Ala Tyr Arg Ala Leu Thr Glu Thr Ile Met Phe Asp			
340	345	350	
gac gcc att gag agg gcg ggc cag ctc acc agc gag gag gac acg ctg		1104	
Asp Ala Ile Glu Arg Ala Gly Gln Leu Thr Ser Glu Glu Asp Thr Leu			
355	360	365	
agc ctc gtc act gcc gac cac tcc cac gtc ttc tcc ttc gga ggc tac		1152	
Ser Leu Val Thr Ala Asp His Ser His Val Phe Ser Phe Gly Gly Tyr			
370	375	380	
ccc ctg cga ggg agc tcc atc ttc ggg ctg gcc cct ggc aag gcc cgg		1200	
Pro Leu Arg Gly Ser Ser Ile Phe Gly Leu Ala Pro Gly Lys Ala Arg			
385	390	395	400
gat cgt aag gcc tac aca gtg cta ctg tat ggc aat ggc cca ggg tat		1248	
Asp Arg Lys Ala Tyr Thr Val Leu Leu Tyr Gly Asn Gly Pro Gly Tyr			
405	410	415	
gtc cta aag gat gga gct aga cca gat gtc aca gag tca gag tct gga		1296	
Val Leu Lys Asp Gly Ala Arg Pro Asp Val Thr Glu Ser Glu Ser Gly			
420	425	430	
tct cca gag tac cgt cag caa tcg gcc gta ccg tta gat gaa gag act		1344	
Ser Pro Glu Tyr Arg Gln Gln Ser Ala Val Pro Leu Asp Glu Glu Thr			
435	440	445	
cac gca ggg gaa gac gtc gct gtc ttt gca aga ggt ccc cag gca cat		1392	
His Ala Gly Glu Asp Val Ala Val Phe Ala Arg Gly Pro Gln Ala His			
450	455	460	
ctc gtg cat ggc gta cag gaa cag act ttc atc gct cat gta atg gca		1440	
Leu Val His Gly Val Gln Glu Gln Thr Phe Ile Ala His Val Met Ala			
465	470	475	480
ttc gca gca tgt ttg gag cca tat acc gct tgc gat tta gct cca cca		1488	
Phe Ala Ala Cys Leu Glu Pro Tyr Thr Ala Cys Asp Leu Ala Pro Pro			
485	490	495	
gca ggt acg aca gac gct gcc cat cca ggt taa		1521	
Ala Gly Thr Thr Asp Ala Ala His Pro Gly			
500	505		

<210> 11
<211> 506
<212> PRT
<213> Homo sapiens

<400> 11

Met Leu Leu Leu Leu Leu Leu Gly Leu Arg Leu Gln Leu Ser Leu

1

5

10

15

Gly Ile Ile Pro Val Glu Glu Glu Asn Pro Asp Phe Trp Asn Arg Glu
20 25 30

Ala Ala Glu Ala Leu Gly Ala Ala Lys Lys Leu Gln Pro Ala Gln Thr
35 40 45

Ala Ala Lys Asn Leu Ile Ile Phe Leu Gly Asp Gly Met Gly Val Ser
50 55 60

Thr Val Thr Ala Ala Arg Ile Leu Lys Gly Gln Lys Lys Asp Lys Leu
65 70 75 80

Gly Pro Glu Ile Pro Leu Ala Met Asp Arg Phe Pro Tyr Val Ala Leu
85 90 95

Ser Lys Thr Tyr Asn Val Asp Lys His Val Pro Asp Ser Gly Ala Thr
100 105 110

Ala Thr Ala Tyr Leu Cys Gly Val Lys Gly Asn Phe Gln Thr Ile Gly
115 120 125

Leu Ser Ala Ala Ala Arg Phe Asn Gln Cys Asn Thr Thr Arg Gly Asn
130 135 140

Glu Val Ile Ser Val Met Asn Arg Ala Lys Lys Ala Gly Lys Ser Val
145 150 155 160

Gly Val Val Thr Thr Arg Val Gln His Ala Ser Pro Ala Gly Thr
165 170 175

Tyr Ala His Thr Val Asn Arg Asn Trp Tyr Ser Asp Ala Asp Val Pro
180 185 190

Ala Ser Ala Arg Gln Glu Gly Cys Gln Asp Ile Ala Thr Gln Leu Ile
195 200 205

Ser Asn Met Asp Ile Asp Val Ile Leu Gly Gly Arg Lys Tyr Met
210 215 220

Phe Pro Met Gly Thr Pro Asp Pro Glu Tyr Pro Asp Asp Tyr Ser Gln
225 230 235 240

Gly Gly Thr Arg Leu Asp Gly Lys Asn Leu Val Gln Glu Trp Leu Ala
245 250 255

Lys Arg Gln Gly Ala Arg Tyr Val Trp Asn Arg Thr Glu Leu Met Gln
260 265 270

Ala Ser Leu Asp Pro Ser Val Thr His Leu Met Gly Leu Phe Glu Pro
275 280 285

Gly Asp Met Lys Tyr Glu Ile His Arg Asp Ser Thr Leu Asp Pro Ser
290 295 300

Leu Met Glu Met Thr Glu Ala Ala Leu Arg Leu Leu Ser Arg Asn Pro
305 310 315 320

Arg Gly Phe Phe Leu Phe Val Glu Gly Gly Arg Ile Asp His Gly His
325 330 335

His Glu Ser Arg Ala Tyr Arg Ala Leu Thr Glu Thr Ile Met Phe Asp
340 345 350

Asp Ala Ile Glu Arg Ala Gly Gln Leu Thr Ser Glu Glu Asp Thr Leu
355 360 365

Ser Leu Val Thr Ala Asp His Ser His Val Phe Ser Phe Gly Gly Tyr
370 375 380

Pro Leu Arg Gly Ser Ser Ile Phe Gly Leu Ala Pro Gly Lys Ala Arg
385 390 395 400

Asp Arg Lys Ala Tyr Thr Val Leu Leu Tyr Gly Asn Gly Pro Gly Tyr
405 410 415

Val Leu Lys Asp Gly Ala Arg Pro Asp Val Thr Glu Ser Glu Ser Gly
420 425 430

Ser Pro Glu Tyr Arg Gln Gln Ser Ala Val Pro Leu Asp Glu Glu Thr
435 440 445

His Ala Gly Glu Asp Val Ala Val Phe Ala Arg Gly Pro Gln Ala His
450 455 460

Leu Val His Gly Val Gln Glu Gln Thr Phe Ile Ala His Val Met Ala
465 470 475 480

Phe Ala Ala Cys Leu Glu Pro Tyr Thr Ala Cys Asp Leu Ala Pro Pro
485 490 495

Ala Gly Thr Thr Asp Ala Ala His Pro Gly
500 505

<210> 12
<211> 1521
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(1518)

<400> 12
atg ctg ctg ctg ctg ctg ggc ctg agg cta cag ctc tcc ctg 48
Met Leu Leu Leu Leu Leu Leu Gly Leu Arg Leu Gln Leu Ser Leu
1 5 10 15

ggc atc atc cca gtt gag gag gag aac ccg gac ttc tgg aac cgc gag 96
Gly Ile Ile Pro Val Glu Glu Asn Pro Asp Phe Trp Asn Arg Glu
20 25 30

gca gcc gag gcc ctg ggt gcc gcc aag aag ctg cag cct gca cag aca 144
Ala Ala Glu Ala Leu Gly Ala Ala Lys Lys Leu Gln Pro Ala Gln Thr
35 40 45

gcc gcc aag aac ctc atc atc ttc ctg ggc gat ggg atg ggg gtg tct 192
Ala Ala Lys Asn Leu Ile Ile Phe Leu Gly Asp Gly Met Gly Val Ser
50 55 60

acg gtg aca gct gcc agg atc cta aaa ggg cag aag gac aaa ctg 240
Thr Val Thr Ala Ala Arg Ile Leu Lys Gly Gln Lys Lys Asp Lys Leu
65 70 75 80

ggg cct gag ata ccc ctg gcc atg gac cgc ttc cca tat gtg gct ctg 288
Gly Pro Glu Ile Pro Leu Ala Met Asp Arg Phe Pro Tyr Val Ala Leu
85 90 95

tcc aag aca tac aat gta gac aaa cat gtg cca gac agt gga gcc aca 336
Ser Lys Thr Tyr Asn Val Asp Lys His Val Pro Asp Ser Gly Ala Thr
100 105 110

gcc acg gcc tac ctg tgc ggg gtc aag ggc aac ttc cag acc att ggc 384
Ala Thr Ala Tyr Leu Cys Gly Val Lys Gly Asn Phe Gln Thr Ile Gly
115 120 125

ttg agt gca gcc gcc cgc ttt aac cag tgc aac acg aca cgc ggc aac 432

Leu Ser Ala Ala Ala Arg Phe Asn Gln Cys Asn Thr Thr Arg Gly Asn
130 135 140

gag gtc atc tcc gtg atg aat cgg gcc aag aaa gca ggg aag tca gtg 480
Glu Val Ile Ser Val Met Asn Arg Ala Lys Lys Ala Gly Lys Ser Val
145 150 155 160

gga gtg gta acc acc aca cga gtg cag cac gcc tcg cca gcc ggc acc 528
Gly Val Val Thr Thr Arg Val Gln His Ala Ser Pro Ala Gly Thr
165 170 175

tac gcc cac acg gtg aac cgc aac tgg tac tcg gac gcc gac gtg cct 576
Tyr Ala His Thr Val Asn Arg Asn Trp Tyr Ser Asp Ala Asp Val Pro
180 185 190

gcc tcg gcc cgc cag gag ggg tgc cag gac atc gct acg cag ctc atc 624
Ala Ser Ala Arg Gln Glu Gly Cys Gln Asp Ile Ala Thr Gln Leu Ile
195 200 205

tcc aac atg gac att gac gtg atc cta ggt gga ggc cga aag tac atg 672
Ser Asn Met Asp Ile Asp Val Ile Leu Gly Gly Arg Lys Tyr Met
210 215 220

ttt cgc atg gga acc cca gac cct gag tac cca gat gac tac agc caa 720
Phe Arg Met Gly Thr Pro Asp Pro Glu Tyr Pro Asp Asp Tyr Ser Gln
225 230 235 240

ggg acc agg ctg gac ggg aag aat ctg gtg cag gaa tgg ctg gcg 768
Gly Gly Thr Arg Leu Asp Gly Lys Asn Leu Val Gln Glu Trp Leu Ala
245 250 255

aag cgc cag ggt gcc cgg tat gtg tgg aac cgc act gag ctc atg cag 816
Lys Arg Gln Gly Ala Arg Tyr Val Trp Asn Arg Thr Glu Leu Met Gln
260 265 270

gct tcc ctg gac ccg tct gtg acc cat ctc atg ggt ctc ttt gag cct 864
Ala Ser Leu Asp Pro Ser Val Thr His Leu